

Table SI. GEO dataset on cervix.

	GSE44001	GSE63514	GSE122697	GSE146114	GSE7803	GSE30760
Platform	GPL14951	GPL570	GPL10558	GPL6884	GPL96	GPL8490
Species	<i>Homo sapiens</i>	<i>Homo sapiens</i>	<i>Homo sapiens</i>	<i>Homo sapiens</i>	<i>Homo sapiens</i>	<i>Homo sapiens</i>
Samples in disease group	300	28	11	83	21	47
Samples in control group	0	24	5	25	10	168
(Ref.)	PMID:2414511 3 (23)	PMID:26056290 (22)	PMID:31229557 (20)	PMID:325801 39 (21)	PMID:179 74957 (25)	PMID: 27103033 (24)

GEO, Gene Expression Omnibus.

Table SII. Lactylation-related genes

ACAT2	ACIN1	ADAR	ADNP	AHNAK	ALB
ALDH1A1	ALDOA	ALDOB	ALYREF	ARGLU1	ARID1A
ARID3A	ARID3B	ARPP19	BCLAF1	BOLA2	BRD4
BTF3	BZW1	BZW2	C19orf53	CACYBP	CALD1
CALM1	CALML5	CALR	CBR1	CBX3	CBX5
CCNA2	CCT5	CD2BP2	CDC5L	CDV3	CDV3
CDYL	CEBPZ	CFDP1	CHD4	CHERP	CNN2
CNN3	COPS4	CRABP2	CSRP1	CSRP2	CWC15
DDX17	DDX18	DDX21	DDX39A	DDX39B	DDX3X
DDX41	DDX42	DDX46	DDX5	DECR1	DFFA
DHRS7	DHX16	DHX9	EAF1	ECHDC1	EDF1
EEF1A1	EEF1G	EEF2	EHMT2	EIF3D	EIF3J
EIF4G1	EIF4G2	EIF4H	EMG1	ENO1	ENSA
FABP5	FAM50A	FKBP3	FLYWCH2	FUBP1	G6PD
GAPDH	GATAD2A	GATAD2B	GFAP	GIGYF2	GTF2F1
GTF2I	H1-2	H1-3	H1-5	H2AFV	H2AFZ
H2AJ	H2AX	H2AZ1	H2AZ2	H2BC13	H2BC14
H2BC18	H2BC5	H2BU1	H3-3A	H3C1	H3C15
H4C1	HCFC1	HDAC1	HDAC2	HDGF	HDGFL2
HEXIM1	HIST1H1C	HIST1H2BB	HIST1H2BD	HIST1H2BH	HIST1H2BK
HIST1H2BL	HIST1H2BN	HIST1H2BO	HIST1H3A	HIST1H4A	HIST2H2BE
HIST2H2BF	HISTIH2BH	HLTF	HMGA1	HMGB1	HMGN1
HMGN2	HMGN3	HMGN4	HNRNPA1	HNRNPC	HNRNPD
HNRNPF	HNRNPH1	HNRNPK	HNRNPL	HNRNPM	HNRNPU
HSDL2	HSPE1	IARS2	IFI16	IK	IKZF1
ILF2	ILF3	IRF2BP2	JMJD1C	JPT1	JPT2
KHDRBS1	KHSRP	KIF2C	KRT1	KRT10	LAP3
LCP1	LDHB	LEMD3	LGALS1	LRPPRC	LSP1
MAGOH	MAGOHB	MAP2K4	MAPRE1	MBD2	MBP
MDC1	MKI67	MNDA	MPHOSPH6	MSN	MTA1
MTA2	MYH13	NCDN	NCL	NEFL	NHLRC2
NOC3L	NOLC1	NONO	NOP2	NPM1	NSUN2
NUCKS1	NUDT21	NUDT5	NUP133	NUP50	PABPC1
PABPN1	PAK2	PARP1	PCBP1	PCBP2	PCMT1
PCNP	PDAP1	PDLIM1	PES1	PFKM	PFKP
PFN1	PGK1	PHC3	PHF6	PKM2	POLDIP3
PPIA	PPIL4	PPM1G	PPP1CB	PPP1CC	PPP1R2B
PRAM1	PRCC	PRDX1	PRKDC	PRPF6	PSMA7
PSMC1	PSME3IP1	PTBP1	PTMA	RACGAP1	RALYL
RAN	RANBP2	RB1	RBM10	RBM14	RBM17
RBM25	RBM39	RBMX	RCC2	RECQL	RFC1

RFC4	RIMS1	RPA1	RPL13	RPL14	RPL22
RPL24	RPL29	RPL5	RPS11	RPS23	RPS27A
RRP1B	RSL1D1	S100A11	S100A4	S100A6	SAFB
SARNP	SATB1	SET	SF3A1	SF3B1	SFPQ
SFPQ	SH3GL1	SMAP	SMARCA5	SMARCC1	SMARCC2
SMC3	SNRPA1	SOD1	SPR	SPR14	SRP14
SRRM1	SRRM2	SSB	STMN1	SUB1	SUMO2
TCOF1	TERF2	THOC2	THRAP3	THUMPD1	TKT
TMA7	TMPO	TMSB4X	TOP2B	TP53	TPM4
TPR	TRIM28	TRIR	TSSC4	U2AF2	U2SURP
UBE2E1	UBE2M	UPF1	VAR5	VIM	WAS
WBP11	WDR33	WIZ	XPO5	XRCC4	YLPM1
ZC3H18	ZC3H4	ZMYM3	ZNF207	ZNF280C	ZNF706
ZNFX1	ZRANB2	ZYX			

Table SIII. siRNA sequences of HMGN1.

Gene	Species	Type	Target sequence (5'-3')
HMGN1	<i>Homo sapiens</i>	NC	F: UUCUCCGAACGUGUCACGUTT
			R: ACGUGACACGUUCGGAGAAUU
		si-1	F: GGAUAAA UCUUCAGACAAA
			R: UUUGUCUGAAGAUUUAUCC
		si-2	F: UGAUGAAGCAGGAGAGAAA
			R:UUUC UCUCCUGCUUCAUCA

siRNA, small interfering RNA; NC, non-targeting control; HMGN1, HMGN1, high-mobility group nucleosome-binding protein 1; F, forward; R, reverse.

Table SIV. Primer sequences for the prediction model of LAGs.

Gene	Primer sequence (5'-3')
FABP5	F: CCAAGCCAGATTGTATCATCAC
	R: CATCAGCTGTGGTTTCTTCAAA
HMG1	F: TGCAAACAAAAGGGAAAAGG
	R: CATCAGAGGCTGGACTCTCC
ZYG	F: CAGCAGTTCTACAGTCTGGAG
	R: GTACTGCTTGTGGTAGTCGG
PAK2	F: GACAGTTACCTGGTAGGAGATG
	R: AACTCCAATGCCTGTAAACAC
PPM1G	F: AACTCCTTCAACAAGAAAATGGC
	R: TGCCTCAAAGAACTTGGACTT
NUP50	F: TAGCTCTGTTTTGGGCTCATT
	R: TGGTGAAGAGACTGGTTTACTC
HDGF	F: TCAACAGCCAACAATACCAAG
	R: TTCTCCTTGGATTCCTCGTAAG
PGK1	F: TTCTGTTCTTGAAGGACTGTGT
	R: CTTAACCTTGTTCCTCCAGAAGC
G6PD	F: TCACCAAGAACATTCACGAGTC
	R: GAAGATCCTGTTGGCAAATCTC
PSMA7	F: CGAAGCCATTGAAACAGATGAT
	R: CAAGTTCAATGTTTTTGCCACC
TCOF1	F: TTTGTCGACCCTAATCGTAGTC
	R: CAGGAGTCAAGCACTGTGTAG
TKT	F: AGAAGATCTGGCTATGTTTCGG
	R: TAGTTCCACTGCCTTCTCTGTA
PFKM	F: TTGTCCATGAGGGTTATCAAGG
	R: ATGACACAGAGATTGGTGATCC
ARID3B	F: GAGAGAAGCCCAGTTCTTGTAT
	R: GAACTCTGGCTAAGGGACCTAA
GAPDH	F: TGAACGGGAAGCTCACTGG
	R: GCTTCACCTTCTTGATGTC

F, forward; R, reverse; HMG1, high-mobility group nucleosome-binding protein 1; NUP50, nucleoporin 50; TKT, transketolase; ZYG, zyxin; PAK2, p21 (RAC1) activated kinase 2; ARID3B, AT-rich interaction domain 3B; FABP5, fatty acid binding protein 5; HDGF, hepatoma-derived growth factor; TCOF1, treacle ribosome biogenesis factor 1; PSMA7, proteasome subunit α type-7; G6PD, glucose-6-phosphate dehydrogenase; PPM1G, protein phosphatase, Mg^{2+}/Mn^{2+} dependent 1G.

Table SV. GO enrichment of the LAG genes.

Ontology	ID	Description	Set size	Enrichment score	NES	P-value	Adjusted P-value	Q-value
CC	GO:0005575	Cellular_component	250	-0.610003226	-2.259097512	0.000368619235033345	0.0190990841151652	0.0151085383832746
CC	GO:0110165	Cellular anatomical entity	250	-0.610003226	-2.259097512	0.000368619235033345	0.0190990841151652	0.0151085383832746
CC	GO:0005925	Focal adhesion	12	-0.574898785	-2.233350264	0.00142592618399868	0.0289685376270729	0.0229158770130994
CC	GO:0030055	Cell-substrate junction	12	-0.574898785	-2.233350264	0.00142592618399868	0.0289685376270729	0.0229158770130994
MF	GO:0070851	Growth factor receptor binding	10	-0.570281124	-2.039315468	0.00286257060056326	0.0388874879204204	0.0307623706106557
BP	GO:0018108	Peptidyl-tyrosine phosphorylation	13	-0.560649651	-2.221782277	0.000897738165294928	0.0258810899181165	0.0204735178959896
BP	GO:0018212	Peptidyl-tyrosine modification	13	-0.560649651	-2.221782277	0.000897738165294928	0.0258810899181165	0.0204735178959896
BP	GO:0018193	Peptidyl-amino acid modification	19	-0.552019	-2.665236512	6.37906576400456e-05	0.0176274850611993	0.0139444139332451
BP	GO:0006959	Humoral immune response	15	-0.524921566	-2.253951294	0.00134824107563652	0.0289685376270729	0.0229158770130994
BP	GO:0051047	Positive regulation of secretion	13	-0.514101422	-2.037317647	0.00346968519469375	0.0429308809910614	0.0339609407116136
BP	GO:1903532	Positive regulation of secretion by cell	13	-0.514101422	-2.037317647	0.00346968519469375	0.0429308809910614	0.0339609407116136
BP	GO:0015833	Peptide transport	15	-0.503573104	-2.162283515	0.00270979776163083	0.0380749549896942	0.030119607591365
MF	GO:0050839	Cell adhesion molecule binding	21	-0.481677687	-2.358934761	0.000285523970355615	0.0190990841151652	0.0151085383832746
BP	GO:0044057	Regulation of system process	17	-0.47360335	-2.151664166	0.00156644437790304	0.0289685376270729	0.0229158770130994
BP	GO:0051046	Regulation of secretion	21	-0.471060102	-2.306936939	0.000485630918620261	0.0211051564602139	0.0166954637479693
BP	GO:0045765	Regulation of angiogenesis	17	-0.466942149	-2.121401147	0.00191240360573444	0.030794537482061	0.0243603540744385
BP	GO:1901342	Regulation of vasculature development	17	-0.466942149	-2.121401147	0.00191240360573444	0.030794537482061	0.0243603540744385
BP	GO:00428	Amide transport	17	-0.466317083	-2.118561362	0.001931623581504	0.0307945374820	0.0243603540744

	86					43	61	385
BP	GO:0030198	Extracellular matrix organization	23	-0.466101695	-2.366092302	0.000305046516738724	0.0190990841151652	0.0151085383832746
BP	GO:0043062	Extracellular structure organization	23	-0.466101695	-2.366092302	0.000305046516738724	0.0190990841151652	0.0151085383832746
BP	GO:0045229	External encapsulating structure organization	23	-0.466101695	-2.366092302	0.000305046516738724	0.0190990841151652	0.0151085383832746
BP	GO:1903530	Regulation of secretion by cell	20	-0.452904105	-2.196384121	0.00144707339435459	0.0289685376270729	0.0229158770130994
BP	GO:0010243	Response to organonitrogen compound	31	-0.430317221	-2.450749756	0.000298494862043224	0.0190990841151652	0.0151085383832746
BP	GO:0007186	G protein-coupled receptor signaling pathway	24	-0.422888701	-2.183217587	0.00102847334279344	0.0280731316439672	0.0222075563636487
BP	GO:0023061	Signal release	22	-0.421005325	-2.119794783	0.00139471267517542	0.0289685376270729	0.0229158770130994
BP	GO:0001666	Response to hypoxia	24	-0.406814545	-2.100232677	0.00173369522231175	0.030794537482061	0.0243603540744385
BP	GO:0006468	Protein phosphorylation	25	-0.405657721	-2.130797523	0.00198412020804384	0.0310346349522328	0.0245502857916844
BP	GO:0016310	Phosphorylation	32	-0.401308745	-2.327745591	0.000336317976653812	0.0190990841151652	0.0151085383832746
BP	GO:0001932	Regulation of protein phosphorylation	23	-0.401286816	-2.037069713	0.00326923397873026	0.0423467963807405	0.0334988942228446
BP	GO:1901698	Response to nitrogen compound	32	-0.396025994	-2.297103595	0.000433098645135801	0.0208807949441789	0.0165179801285295
MF	GO:00140677	Molecular function activator activity	42	-0.391354568	-2.458935753	0.000222416498355495	0.0190990841151652	0.0151085383832746
MF	GO:0030546	Signaling receptor activator activity	35	-0.389973678	-2.331447763	0.000534630018895647	0.0211051564602139	0.0166954637479693
MF	GO:0048018	Receptor ligand activity	35	-0.389973678	-2.331447763	0.000534630018895647	0.0211051564602139	0.0166954637479693
BP	GO:0032940	Secretion by cell	26	-0.388650996	-2.074502267	0.00157247791703049	0.0289685376270729	0.0229158770130994
BP	GO:00140352	Export from cell	26	-0.388650996	-2.074502267	0.00157247791703049	0.0289685376270729	0.0229158770130994
BP	GO:0022603	Regulation of anatomical structure morphogenesis	32	-0.385252239	-2.23461166	0.00068568336576507	0.0236846462591351	0.0187359972312122
BP	GO:00071	Transmembrane receptor protein tyrosine kinase	26	-0.382513779	-2.041743647	0.002279393735341	0.0337431679749	0.0266929003217

	69	signaling pathway				43	651	615
BP	GO:0 0469 03	Secretion	34	-0.37934 9	-2.2494 78028	0.0009053 69852382 845	0.025881 0899181 165	0.020473 5178959 896
BP	GO:0 0082 84	Positive regulation of cell population proliferation	30	-0.37447 1534	-2.1060 292	0.0018355 65238628 82	0.030794 5374820 61	0.024360 3540744 385
BP	GO:0 0723 59	Circulatory system development	49	-0.37226 6434	-2.4948 7058	0.0001077 55068331 11	0.019099 0841151 652	0.015108 5383832 746
BP	GO:0 0717 05	Nitrogen compound transport	33	-0.36854 9712	-2.1669 86567	0.0012662 52185451 63	0.028968 5376270 729	0.022915 8770130 994
BP	GO:0 0352 95	Tube development	48	-0.36406 9274	-2.4029 34663	0.0001690 03714689 838	0.019099 0841151 652	0.015108 5383832 746
BP	GO:0 0164 77	Cell migration	57	-0.35736 4393	-2.4656 36859	4.7983972 6258771e- 05	0.017627 4850611 993	0.013944 4139332 451
BP	GO:0 0488 70	Cell motility	57	-0.35736 4393	-2.4656 36859	4.7983972 6258771e- 05	0.017627 4850611 993	0.013944 4139332 451
MF	GO:0 0305 45	Signaling receptor regulator activity	38	-0.33860 9905	-2.1112 32839	0.0021805 61624101 22	0.032867 0106614 53	0.025999 8065419 151
BP	GO:0 0714 95	Cellular response to endogenous stimulus	43	-0.33764 3324	-2.1219 61688	0.0010497 79349774 41	0.028073 1316439 672	0.022207 5563636 487
BP	GO:0 0067 93	Phosphorus metabolic process	48	-0.33517 2079	-2.2122 07032	0.0008040 76091188 438	0.025637 6569075 083	0.020280 9475631 74
BP	GO:0 0067 96	Phosphate-containing compound metabolic process	48	-0.33517 2079	-2.2122 07032	0.0008040 76091188 438	0.025637 6569075 083	0.020280 9475631 74
BP	GO:0 0019 44	Vasculature development	41	-0.33496 3779	-2.1097 46613	0.0017820 97821468 82	0.030794 5374820 61	0.024360 3540744 385
BP	GO:1 9017 01	Cellular response to oxygen-containing compound	41	-0.31889 8098	-2.0085 58017	0.0036646 11329227 1	0.044675 9234107 246	0.035341 3755125 153
BP	GO:2 0000 26	Regulation of multicellular organismal development	51	-0.31208 3038	-2.0913 75325	0.0020759 73775330 15	0.031870 0418471 981	0.025211 1435093 701
MF	GO:0 0987 72	Molecular function regulator activity	62	-0.31042 3769	-2.1977 17992	0.0006656 49321563 047	0.023684 6462591 351	0.018735 9972312 122
BP	GO:0 0096 53	Anatomical structure morphogenesis	77	-0.29457 9975	-2.2413 77601	0.0004533 82761152 255	0.020880 7949441 789	0.016517 9801285 295
BP	GO:0 0512 40	Positive regulation of multicellular organismal process	54	-0.29322 4096	-1.9924 7699	0.0024930 25595369 5	0.036258 2143607 248	0.028682 4551415 549
BP	GO:1 9017 00	Response to oxygen-containing compound	58	-0.29265 7295	-2.0354 49685	0.0014514 33206789 15	0.028968 5376270 729	0.022915 8770130 994
MF	GO:0 0051	Signaling receptor binding	56	-0.28899 8607	-1.9835 92263	0.0025676 54301403	0.036699 7485493	0.029031 7355675

	02					34	685	913
BP	GO:0071310	Cellular response to organic substance	56	-0.287918853	-1.976181183	0.00282657160916653	0.0388874879204204	0.0307623706106557
MF	GO:0005515	Protein binding	208	-0.286514494	-2.010699109	0.00140098784063613	0.0289685376270729	0.0229158770130994
BP	GO:0009719	Response to endogenous stimulus	57	-0.278453166	-1.921188576	0.00290835253445846	0.0388874879204204	0.0307623706106557
BP	GO:0048518	Positive regulation of biological process	117	-0.272234936	-2.235745802	0.000350647514200826	0.0190990841151652	0.0151085383832746
BP	GO:0006950	Response to stress	90	-0.271057513	-2.116408377	0.00062976207501403	0.0236846462591351	0.0187359972312122
BP	GO:0048731	System development	92	-0.261508366	-2.044869392	0.00186296029086618	0.030794537482061	0.0243603540744385
BP	GO:0050896	Response to stimulus	161	-0.261151511	-2.108011403	0.0012232064742139	0.0289685376270729	0.0229158770130994
BP	GO:0070887	Cellular response to chemical stimulus	80	-0.253171531	-1.963502997	0.00308528936832333	0.0405984902593657	0.0321158776351785
BP	GO:0051716	Cellular response to stimulus	135	-0.251620483	-2.08578835	0.00143039778187006	0.0289685376270729	0.0229158770130994
BP	GO:0042221	Response to chemical	106	-0.246844474	-1.991616811	0.00154280672586062	0.0289685376270729	0.0229158770130994
BP	GO:0050794	Regulation of cellular process	168	-0.244681156	-1.954250665	0.00341820469747849	0.0429308809910614	0.0339609407116136
BP	GO:0044255	Cellular lipid metabolic process	25	0.464925772106875	2.27588130241744	0.000270386732338723	0.0190990841151652	0.0151085383832746

GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function; LAG, lactylation-related genes; ID, identifier.